

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:27:47 ; Search time 42 Seconds (without alignments)

58.653 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: KNESSNTATNTKQWKRDETKGRDEAKRFKNTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : Issued_Patents_AA:^{*}

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 3: /cggn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cggn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
 6: /cggn2_6/ptodata/1/iaa/backfiles1.comb.pep:
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RESULTS

RESULT 1
 US-09-328-352-6545
 ; Sequence 6545, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BRUANII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO: 6545
 ; LENGTH: 72
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ;
 US-09-328-352-6545

Query Match 31.2%; Score 55; DB 4; Length 72;
 Best Local Similarity 48.0%; Pred. No. 0.9;
 Matches 12; Conservative 3; Mismatches 6; Deletes 4; Gaps 1;

Qy 6 TNATNTKQWKRDETKGRDEAK 26
 Db 3 SNTTGTWKWNETKGRGFIQTDEGK 27

RESULT 2
 US-09-106-164-2
 ; Sequence 2, Application US/09106464
 ; Patent No. 601145
 ; GENERAL INFORMATION:
 ; APPLICANT: Steffens, John C.
 ; APPLICANT: Changas, Gurdev S.
 ; APPLICANT: Kua, Jian-Pang
 ; APPLICANT: Eannetta, Nancy
 ; TITLE OF INVENTION: Chain Length Specific UDP-Glc:Fatty Acid
 ; TITLE OF INVENTION: Glucosyltransferases
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Jones, Tullar & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22200
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	55	31.2	72	4	US-09-328-352-6545	Sequence 6545, Ap	Sequence 6545, Ap
2	55	31.2	471	3	US-09-106-464-2	Sequence 2, Appli	Sequence 2, Appli
3	53	30.1	277	4	US-09-134-000C-4173	Sequence 4173, Ap	Sequence 4173, Ap
4	52	29.5	75	4	US-09-343-681A-7857	Sequence 7857, Ap	Sequence 7857, Ap
5	51.5	29.3	1094	3	US-09-268-347-32	Sequence 32, Appli	Sequence 32, Appli
6	51	29.0	165	3	US-09-965-682A-3	Sequence 3, Appli	Sequence 3, Appli
7	51	29.0	165	3	US-09-359-967-3	Sequence 2, Appli	Sequence 2, Appli
8	51	29.0	165	4	US-09-538-092-1224	Sequence 1224, Ap	Sequence 1224, Ap
9	51	29.0	165	4	US-09-948-000C-4173	Sequence 6345, Ap	Sequence 6345, Ap
10	51	29.0	166	2	US-08-918-723-4	Sequence 4, Appli	Sequence 4, Appli
11	51	29.0	166	2	US-09-237-507-4	Sequence 3, Appli	Sequence 3, Appli
12	51	29.0	176	4	US-09-949-016-8150	Sequence 2, Appli	Sequence 2, Appli
13	51	29.0	238	4	US-09-377-285B-2	Sequence 4, Appli	Sequence 4, Appli
14	51	29.0	354	4	US-09-377-285B-4	Sequence 26, Appli	Sequence 26, Appli
15	51	29.0	354	4	US-09-377-285B-26	Sequence 36, Appli	Sequence 36, Appli
16	51	29.0	354	4	US-09-377-285B-36	Sequence 38, Appli	Sequence 38, Appli
17	51	29.0	366	4	US-09-377-285B-38	Sequence 2, Appli	Sequence 2, Appli
18	51	29.0	455	3	US-09-130-339-2	Sequence 755, Ap	Sequence 755, Ap
19	50	28.4	96	4	US-09-621-976-7575	Sequence 756, Ap	Sequence 756, Ap
20	50	28.4	106	4	US-09-621-976-7576	Sequence 757, Ap	Sequence 757, Ap
21	50	28.4					

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/09/106,464
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 670/055,554
; FILING DATE: 13-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Spector, Eric S.
; REGISTRATION NUMBER: 22495
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQ ID NO: 106-464-2

RESULT 3
US-09-134-000C-4173
Sequence 4173, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 0322796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4173
LENGTH: 277
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4173

Query Match 30.1%
Best Local Similarity 34.6%
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Score 53; DB 4; Length 277;
Qy 7 NATNTKQWDTKGFRDEAKRFKNTA 32
Db 108 NEESTKQWDTKKEYQESSEKERQKQSA 133

RESULT 4
US-09-543-681A-7857
Sequence 7857, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

; PRIORITY: Filing date 13-AUG-1997
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 7857
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7857

Query Match 29.5%
Best Local Similarity 50.0%
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Score 52; DB 4; Length 75;
Qy 2 NESSTNTATNTKQWDTKGFR 21
Db 4 NSMSNSMTGIVKWFDEKGKF 23

RESULT 5
US-09-268-347-32
Sequence 32, Application US/09268347
Patent No. 6325182
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 32
LENGTH: 1094
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-268-347-32

Query Match 29.3%
Best Local Similarity 37.5%
Matches 12; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
Score 51.5; DB 3; Length 1094;
Qy 3 ESSNTNTATNTKQWDTKGFRDEAKRFKN-TAG 33
Db 365 ETVINAVNKGWRKTTGANNQAGKFETVTSG 396

RESULT 6
US-08-965-689A-3
Sequence 3, Application US/08965689A
Patent No. 6015702
GENERAL INFORMATION:
APPLICANT: La, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,689A
APPLICATION NUMBER: 435
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/09/543,681A
APPLICATION NUMBER: 08/933,750
FILING DATE: September 23, 1997
; PRIORITY: Filing date 13-AUG-1997
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 7857
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7857
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

```

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX: 650-845-4166
 REFERENCE/DOCKET NUMBER: PP-0356-1 CIP

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 165 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: 2456290

US-08-965-689A-3

Query Match 29.0%; Score 51; DB 3; Length 165;
 Best Local Similarity 38.5%; Pred. No. 8.9;
 Matches 10; Conservative 5; MisMatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
 Db 132 DESGANVDAASKWRRDREQFYKIAKQ 157

RESULT 8
 US-09-538-092-1224
 Sequence 1224, Application US/09538092
 Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Giot, Loic
 APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 15966-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SEQ ID NO 1224
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0) : (0)
 OTHER INFORMATION: Polypeptide Accession Number P56554
 US-09-538-092-1224

Query Match 29.0%; Score 51; DB 4; Length 165;
 Best Local Similarity 38.5%; Pred. No. 8.9;
 Matches 10; Conservative 5; MisMatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
 Db 132 DESGANVDAASKWRRDREQFYKIAKQ 157

RESULT 9
 US-09-949-016-0345
 Sequence 6345, Application US/09949016
 Patent No. 6812319
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-05-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6345
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Human

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 08/933,750
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX: 650-845-4166
 REFERENCE/DOCKET NUMBER: PP-0356-1 CIP

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 165 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-949-016-6345
 Query Match 29.0%: Score 51; DB 4; Length 165;
 Best Local Similarity 38.5%; Pred. No. 8.9;
 Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Qy 2 NESSTNATNTKWRDDETGFRDEAKR 27
 Db 132 DESPANVAAKWRDK--RDEFKK 157

RESULT 10
 US-08-918-723-4
 Sequence 4, Application US/08918723
 ; Patent No. 5863779
 / GENERAL INFORMATION:
 / APPLICANT: Lal, Preeti
 / ATTORNEY: Corley, Neil C.
 / TITLE OF INVENTION: UBC7-LIKE UBIQUITIN-CONJUGATING ENZYME
 / NUMBER OF SEQUENCES: 4
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Drive
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/918,723
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/918,723
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Billings, Lucy J.
 / REGISTRATION NUMBER: 36,749
 / REFERENCE/DOCKET NUMBER: PF-0368 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-855-0555
 / TELEFAX: 415-845-4166
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 166 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: GenBank
 / CLONE: 992704
 / US-08-918-723-4

Query Match 29.0%: Score 51; DB 2; Length 166;
 Best Local Similarity 42.3%; Pred. No. 9;
 Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 1;
 Qy 2 NESSTNATNTKWRDDETGFRDEAKR 27
 Db 132 DESPANVAAKWRDK--RDEFKK 153

RESULT 11
 US-09-949-016-8150
 Sequence 8150, Application US/0949016
 ; Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / PRIOR APPLICATION NUMBER: 6812339
 / PRIOR FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSEQ for Windows Version 4.0

RESULT 11-507-4
 US-09-237-507-4
 Sequence 4, Application US/09237507
 ; Patent No. 5922181
 / GENERAL INFORMATION:
 / APPLICANT: Lal, Preeti
 / ATTORNEY: Corley, Neil C.
 / TITLE OF INVENTION: UBC7-LIKE UBIQUITIN-CONJUGATING ENZYME
 / NUMBER OF SEQUENCES: 4
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Drive
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/237,507
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/918,723
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Billings, Lucy J.
 / REGISTRATION NUMBER: 36,749
 / REFERENCE/DOCKET NUMBER: PF-0368 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-855-0555
 / TELEFAX: 415-845-4166
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 166 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: GenBank
 / CLONE: 992704
 / US-09-237-507-4

US-09-949-016-8150

Query Match 29.0%; Score 51; DB 4; Length 176;
Best Local Similarity 38.5%; Pred. No. 9.6;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
SEQ ID NO 4

Qy 2 NESSNTNATNTKQWRTDETKGPFDEAKR 27
Db 143 DESGANVADSKMWRDDREQFYKIAKQ 168

RESULT 13
US-09-377-285B-2
Sequence 2, Application US/09377285B
Patent No. 6720175

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: WORLEY, Paul
APPLICANT: TU, Jian
APPLICANT: XIAO, Bo
APPLICANT: BENKEN, Jutta
APPLICANT: LEAHY, Daniel
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
FILE REFERENCE: JHU1580-4
CURRENT APPLICATION NUMBER: US/09/377,285B
PRIORITY FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/138,426
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,493
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/097,334
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2

LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-377-285B-2

Query Match 29.0%; Score 51; DB 4; Length 238;
Best Local Similarity 33.3%; Pred. No. 14;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
SEQ ID NO 26

Qy 7 NATNTKQWRTDETKGPFDEAKR 27
Db 204 STANVKQWQQLAAQEEAER 224

RESULT 14
US-09-377-285B-4
Sequence 4, Application US/09377285B
Patent No. 6720175

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: WORLEY, Paul
APPLICANT: TU, Jian
APPLICANT: XIAO, Bo
APPLICANT: BENKEN, Jutta
APPLICANT: LEAHY, Daniel
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
FILE REFERENCE: JHU1580-4
CURRENT APPLICATION NUMBER: US/09/377,285B
PRIORITY FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/138,426
PRIORITY FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,493
PRIORITY FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIORITY FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26

LENGTH: 354
TYPE: PRT
ORGANISM: Mus musculus
US-09-377-285B-26

Query Match 29.0%; Score 51; DB 4; Length 354;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
SEQ ID NO 26

Qy 7 NATNTKQWRTDETKGPFDEAKR 27
Db 204 STANVKQWQQLAAQEEAER 224

Search completed: March 30, 2005, 14:38:44
Job time: 43 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:31:07 ; Search time 138 Seconds (without alignments)

Perfect score: 176

Sequence: 1 KNESSTNATNTKWRDETKGFRDEAKRFKNTAG 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/prodata/2/pubpaas/US07_PUBCOMB.pep:
2: /cgn2_6/ptodata/2/pubpaas/FCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/2/pubpaas/US06_NEW_PUB.pep:
4: /cgn2_6/prodata/2/pubpaas/US07_PUBCOMB.pep:
5: /cgn2_6/ptodata/2/pubpaas/US07_PUBCOMB.pep:
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9: /cgn2_6/ptodata/2/pubpaas/US09A_PUBCOMB.pep:
10: /cgn2_6/prodata/2/pubpaas/US09B_PUBCOMB.pep:
11: /cgn2_6/ptodata/2/pubpaas/US09C_PUBCOMB.pep:
12: /cgn2_6/prodata/2/pubpaas/US09_NEW_PUB.pep:
13: /cgn2_6/prodata/2/pubpaas/US10A_PUBCOMB.pep:
14: /cgn2_6/prodata/2/pubpaas/US10B_PUBCOMB.pep:
15: /cgn2_6/prodata/2/pubpaas/US10C_PUBCOMB.pep:
16: /cgn2_6/prodata/2/pubpaas/US10D_PUBCOMB.pep:
17: /cgn2_6/ptodata/2/pubpaas/US10_NEW_PUB.pep:
18: /cgn2_6/prodata/2/pubpaas/US11_NEW_PUB.pep:
19: /cgn2_6/prodata/2/pubpaas/US60_NEW_PUB.pep:
20: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-444-662-8

Sequence 8, Application US-10444662
Publication No. US20030220264A1
GENERAL INFORMATION:
APPLICANT: Mirus Corporation
APPLICANT: Rozema, David
APPLICANT: Wolff, Jon
APPLICANT: Wakerfield, Darren
APPLICANT: Ekena, Kirk
APPLICANT: Hagstrom, James
TITLE OF INVENTION: Reversible Modification of Membrane Interaction
FILE REFERENCE: Mirus 035.01
CURRENT APPLICATION NUMBER: US-10/444,662
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 33
TYPE: PRT
ORGANISM: Bacteriophage T7
US-10-444-662-8

Query Match 8, Application US-10-444-662-8
Best Local Similarity 100.0%; Score 176; DB 15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKWRDETKGFRDEAKRFKNTAG 33
Db 1 KNESSTNATNTKWRDETKGFRDEAKRFKNTAG 33

RESULT 2
US-10-633-808-1
Sequence 1, Application US-10633808
Publication No. US20040029326A1

Result No. Score Query Match Length DB ID Description

1 176 100.0 33 15 US-10-444-662-8 Sequence 8, Appli
2 176 100.0 33 15 US-10-633-808-1 Sequence 1, Appli
3 176 100.0 33 15 US-10-633-808-22 Sequence 22, Appli
4 176 100.0 33 15 US-10-633-808-23 Sequence 23, Appli
5 176 100.0 33 15 US-10-633-808-36 Sequence 36, Appli
6 176 100.0 40 15 US-10-633-808-16 Sequence 16, Appli
7 176 100.0 160 15 US-10-633-808-5 Sequence 5, Appli
8 176 100.0 309 15 US-10-633-808-6 Sequence 6, Appli
9 176 100.0 424 15 US-10-633-808-7 Sequence 7, Appli
10 176 100.0 573 15 US-10-633-808-4 Sequence 4, Appli
11 173 98.3 33 15 US-10-633-808-14 Sequence 14, Appli
12 173 98.3 33 15 US-10-633-808-15 Sequence 15, Appli
13 173 98.3 33 16 US-10-782-075-7 Sequence 7, Appli

SUMMARIES

GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wong, So
 ; APPLICANT: Wakefield, Darren
 ; APPLICANT: Sokoloff, Alex
 ; APPLICANT: Monahan, Sean
 ; APPLICANT: Sebestyen, Magdalna
 ; APPLICANT: Wolff, Jon
 ; APPLICANT: Higgs, Lori
 ; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 ; FILE REFERENCE: Mirus.014.06
 ; CURRENT APPLICATION NUMBER: US/10/633.808
 ; CURRENT FILING DATE: 2003-08-04
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage T7
 ; US-10-633-808-1

Query Match 100.0%; Score 176; DB 15; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
 US-10-633-808-23
 ; Sequence 23, Application US/10633808
 ; Publication No. US20040029826A1

GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wong, So
 ; APPLICANT: Wakefield, Darren
 ; APPLICANT: Sokoloff, Alex
 ; APPLICANT: Monahan, Sean
 ; APPLICANT: Sebestyen, Magdalna
 ; APPLICANT: Wolff, Jon
 ; APPLICANT: Higgs, Lori
 ; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 ; FILE REFERENCE: Mirus.014.06
 ; CURRENT APPLICATION NUMBER: US/10/633.808
 ; CURRENT FILING DATE: 2003-08-04
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 36
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage T7
 ; US-10-633-808-23

Query Match 100.0%; Score 176; DB 15; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-10-633-808-16
 ; Sequence 16, Application US/10633808
 ; Publication No. US20040029826A1

GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wong, So
 ; APPLICANT: Wakefield, Darren
 ; APPLICANT: Sokoloff, Alex
 ; APPLICANT: Monahan, Sean
 ; APPLICANT: Sebestyen, Magdalna
 ; APPLICANT: Wolff, Jon
 ; APPLICANT: Higgs, Lori
 ; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 ; FILE REFERENCE: Mirus.014.06
 ; CURRENT APPLICATION NUMBER: US/10/633.808
 ; CURRENT FILING DATE: 2003-08-04
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 36
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage T7
 ; US-10-633-808-16

Query Match 100.0%; Score 176; DB 15; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-10-633-808-22
 ; Sequence 22, Application US/10633808
 ; Publication No. US20040029826A1

GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wong, So
 ; APPLICANT: Wakefield, Darren
 ; APPLICANT: Sokoloff, Alex
 ; APPLICANT: Monahan, Sean
 ; APPLICANT: Sebestyen, Magdalna
 ; APPLICANT: Wolff, Jon
 ; APPLICANT: Higgs, Lori
 ; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 ; FILE REFERENCE: Mirus.014.06
 ; CURRENT APPLICATION NUMBER: US/10/633.808
 ; CURRENT FILING DATE: 2003-08-04
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage T7
 ; US-10-633-808-22

Query Match 100.0%; Score 176; DB 15; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-10-633-808-23
 ; Sequence 23, Application US/10633808
 ; Publication No. US20040029826A1

GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wong, So
 ; APPLICANT: Wakefield, Darren
 ; APPLICANT: Sokoloff, Alex
 ; APPLICANT: Monahan, Sean
 ; APPLICANT: Sebestyen, Magdalna
 ; APPLICANT: Wolff, Jon
 ; APPLICANT: Higgs, Lori
 ; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO

FILE REFERENCE: Mirus .014.06
 CURRENT APPLICATION NUMBER: US/10/633,808
 CURRENT FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 16
 LENGTH: 40
 TYPE: PRT
 ORGANISM: Bacteriophage T7
 US-10-633-808-16

Query Match Score 176; DB 15; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.3e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-10-633-808-5
 Sequence 5, Application US/10633808
 Publication No. US2004029826A1
 GENERAL INFORMATION:
 APPLICANT: Mirus Corporation
 ATTORNEY: Wong, So
 APPLICANT: Wakefield, Darren
 APPLICANT: Sokoloff, Alex
 APPLICANT: Monahan, Sean
 APPLICANT: Sebestyen, Magdalna
 APPLICANT: Wolff, Jon
 APPLICANT: Higgs, Lori
 TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 FILE REFERENCE: Mirus .014.06
 CURRENT APPLICATION NUMBER: US/10/633,808
 CURRENT FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 5
 LENGTH: 160
 TYPE: PRT
 ORGANISM: Bacteriophage T7
 US-10-633-808-5

Query Match Score 176; DB 15; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-10-633-808-6
 Sequence 6, Application US/10633808
 Publication No. US2004029826A1
 GENERAL INFORMATION:
 APPLICANT: Mirus Corporation
 ATTORNEY: Wong, So
 APPLICANT: Wakefield, Darren
 APPLICANT: Sokoloff, Alex
 APPLICANT: Monahan, Sean
 APPLICANT: Sebestyen, Magdalna
 APPLICANT: Wolff, Jon
 APPLICANT: Higgs, Lori
 TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 FILE REFERENCE: Mirus .014.06
 CURRENT APPLICATION NUMBER: US/10/633,808
 CURRENT FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.1

SEQ ID NO: 6
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Bacteriophage T7
 US-10-633-808-6

Query Match Score 176; DB 15; Length 309;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSNTATNTKQWDETKGFRDEAKRFKNTAG 33
 Db 206 KNESSNTATNTKQWDETKGFRDEAKRFKNTAG 238

RESULT 9
 US-10-633-808-7
 Sequence 7, Application US/10633808
 Publication No. US2004029826A1
 GENERAL INFORMATION:
 APPLICANT: Mirus Corporation
 ATTORNEY: Wong, So
 APPLICANT: Wakefield, Darren
 APPLICANT: Sokoloff, Alex
 APPLICANT: Monahan, Sean
 APPLICANT: Sebestyen, Magdalna
 APPLICANT: Wolff, Jon
 APPLICANT: Higgs, Lori
 TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 FILE REFERENCE: Mirus .014.06
 CURRENT APPLICATION NUMBER: US/10/633,808
 CURRENT FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 7
 LENGTH: 424
 TYPE: PRT
 ORGANISM: Bacteriophage T7
 US-10-633-808-7

Query Match Score 176; DB 15; Length 424;
 Best Local Similarity 100.0%; Pred. No. 7e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSNTATNTKQWDETKGFRDEAKRFKNTAG 33
 Db 57 KNESSNTATNTKQWDETKGFRDEAKRFKNTAG 89

RESULT 10
 US-10-633-808-4
 Sequence 4, Application US/10633808
 Publication No. US2004029826A1
 GENERAL INFORMATION:
 APPLICANT: Mirus Corporation
 ATTORNEY: Wong, So
 APPLICANT: Wakefield, Darren
 APPLICANT: Sokoloff, Alex
 APPLICANT: Monahan, Sean
 APPLICANT: Sebestyen, Magdalna
 APPLICANT: Wolff, Jon
 APPLICANT: Higgs, Lori
 TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
 FILE REFERENCE: Mirus .014.06
 CURRENT APPLICATION NUMBER: US/10/633,808
 CURRENT FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 4
 LENGTH: 573
 TYPE: PRT
 ORGANISM: Bacteriophage T7
 US-10-633-808-4

Query Match 100.0%; Score 176; DB 15; Length 573;
Best Local Similarity 100.0%; Pred. No. 9.7e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 206 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33

Qy 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33
Db 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33

RESULT 13
US-10-782-075-7
; Sequence 7, Application US/10782075
; Publication No. US20040167090A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Monahan, Sean
; APPLICANT: Budker, Vladimir
; APPLICANT: Nader, Lisa
; APPLICANT: Subbotin, Vladimir
; APPLICANT: Wolff, Jon A
; TITLE OF INVENTION: Covalent Modification of RNA for In Vitro and In Vivo Delivery
; FILE REFERENCE: Mirus 030 16 6
; CURRENT APPLICATION NUMBER: US/10/782,075
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Bacteriophage T7
; LENGTH: 33
; US-10-782-075-7

Query Match 98.3%; Score 173; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.1e-16;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33
Db 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33

RESULT 14
US-10-633-808-25
; Sequence 25, Application US/10633808
; Publication No. US2004029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdalna
; APPLICANT: Higgs, Lori
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdalna
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus 014 06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bacteriophage T7
; US-10-633-808-25

Query Match 97.7%; Score 172; DB 15; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33
Db 1 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33

RESULT 15
US-10-633-808-26
; Sequence 15, Application US/10633808
; Publication No. US2004009826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdalna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus 014 06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bacteriophage T7
; US-10-633-808-15

Query Match 98.3%; Score 173; DB 15; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.1e-16;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 206 KNESSATNTKQWRDETKGFRDEAKRFPNTAG 33

```

Sequence 26, Application US/10633808
Sequence 26, Application US/10633808
Publication No. US20040029826A1
GENERAL INFORMATION:
APPLICANT: Mirus Corporation
APPLICANT: Wong, So
APPLICANT: Wakefield, Darren
APPLICANT: Sokoloff, Alex
APPLICANT: Monahan, Sean
APPLICANT: Sebestyen, Magdolna
APPLICANT: Wolff, Jon
APPLICANT: Higbee, Lori
TITLE OF INVENTION: A COMPOUND FOR TARGETTING TO HEPATOCYTES IN VIVO
FILE REFERENCE: Mirus.014.06
CURRENT APPLICATION NUMBER: US/10/633,808
CURRENT FILING DATE: 2003-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 33
TYPE: PRT
ORGANISM: Bacteriophage T7
US-10-633-808-26

Query Mat 94.9%; Score 167; DB 15; Length 33;
Best Local Similarity 90.9%; Pred. No. 7.4e-16;
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0
Qry 1 KNESSNTATNTKQWRFDEAKFRKFTAG 33
Db 1 RNESSNTATNTKQWRFDEAKFRKFTAG 33

```

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CC is related to the invention.
 XX Sequence 33 AA;

Query Match 100.0%; Score 176; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.1e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS 1 KNESSNTNNTKQWRDETKGFRDEAKRFKNTAG 33
 Db 1 KNESSNTNNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 2
 ADJ46278
 ID ADJ46278 standard; peptide; 33 AA.
 XX
 AC ADJ46278;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE T7 p17 rod domain peptide, SEQ ID 1.
 XX
 KW Hepatocyte delivery; T7; p17 rod domain.
 XX
 OS Enterobacteria phage T7.
 XX
 PN WO2004013307-A2.

XX
 PD 12-FEB-2004.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.
 XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdko J, Higgs L;
 PI Wakefield D, Sebestyen MG;
 XX
 DR WPI: 2004-203636/19.
 XX
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a T7 derived peptide, such as T7 p17 rod domain (ADJ46278).
 XX
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a T7 derived peptide, such as T7 p17 rod domain (ADJ46278).
 XX
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a T7 derived peptide, such as T7 p17 rod domain (ADJ46278).
 XX
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a T7 derived peptide, such as T7 p17 rod domain (ADJ46278).
 XX
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a T7 derived peptide, such as T7 p17 rod domain (ADJ46278).
 XX
 PS Claim 12; Page 2; 56pp; English.

CC The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-CC ADJ46313 are synthetic peptides derived from the T7 phage p17 protein CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not CC disrupt hepatocyte targeting, and ADJ4602-ADJ46313 have amino acid CC changes which do disrupt hepatocyte targeting.
 XX Sequence 33 AA;

CC Query Match 100.0%; Score 176; DB 8; Length 33;
 CC Best Local Similarity 100.0%; Pred. No. 7.1e-19;
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sequence 33 AA;

CC Query Match 100.0%; Score 176; DB 8; Length 33;
 CC Best Local Similarity 100.0%; Pred. No. 7.1e-19;
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sequence 33 AA;

CC Query Match 100.0%; Score 176; DB 8; Length 33;
 CC Best Local Similarity 100.0%; Pred. No. 7.1e-19;
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sequence 33 AA;

AC ADJ46313;
 XX DT 06-MAY-2004 (first entry)

XX
 DE T7 phage p17 protein ligand-related peptide, SEQ ID 36.
 XX
 KW Hepatocyte delivery; T7; p17 rod domain.
 XX
 OS Enterobacteria phage T7.
 XX
 OS Synthetic.

XX
 Key Location/Qualifiers
 PT Misc-difference 1. .33
 PT /note= "All D-form residues"
 XX
 PN WO2004013307-A2.

XX
 PD 12-FEB-2004.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PA (MIRU-) MIRUS CORP.

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 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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XX
 PR 04-AUG-2003; 2003WO-US024516.

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 PR 05-AUG-2002; 2002US-0401167P.

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 PR 04-AUG-2003; 2003US-00633808.

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XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

XX
 PA (MIRU-) MIRUS CORP.

XX
 PR 04-AUG-2003; 2003WO-US024516.

XX
 PR 05-AUG-2002; 2002US-0401167P.

XX
 PR 04-AUG-2003; 2003US-00633808.

CC cellular internalization pathways which allows more flexibility in
 CC designing delivery strategies and is useful for delivering therapeutic
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present
 CC sequence is the predicted sequence of a fragment of the T7 p17 protein.
 XX

SQ Sequence 309 AA;

Query Match 100.0%; Score 176; DB 8; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

Pf 206 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 238

RESULT 7

ADJ46284 ADJ46284 standard; protein; 424 AA.

XX

AC ADJ46284;

XX

DT 06-MAY-2004 (first entry)

XX

DB T7 p17 protein fragment 150-553, SEQ ID 7.

XX

KW Hepatocyte delivery; T7; p17 rod domain.

XX

OS Enterobacteria phage T7.

XX

PN WO2004013307-A2.

XX

PD 12-FEB-2004.

XX

PP 04-AUG-2003; 2003WO-US024516.

XX

PR 05-AUG-2002; 2002US-0401167P.

XX

PR 04-AUG-2003; 2003US-00633808.

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

CC designing delivery strategies and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present

CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 424 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 424;

XX

Best Local Similarity 100.0%; Pred. No. 1.6e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

Db 57 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 89

XX

CC RESULT 8

ADJ46281

ID ADJ46281 standard; protein; 573 AA.

XX

AC ADJ46281;

XX

DT 06-MAY-2004 (first entry)

XX

DB T7 p17 protein, SEQ ID 4.

XX

KW Hepatocyte delivery; T7; p17 rod domain.

XX

OS Enterobacteria phage T7.

XX

OS Synthetic.

CC cellular internalization pathways which allows more flexibility in
 CC designing delivery strategies and is useful for delivering therapeutic
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present
 CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 309 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 309;

XX

Best Local Similarity 100.0%; Pred. No. 1.1e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Db 206 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

CC designing delivery strategies and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present

CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 424 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 573;

XX

Best Local Similarity 100.0%; Pred. No. 2.3e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

Db 206 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 238

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 25-26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

CC designing delivery strategies and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present

CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 573 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 573;

XX

Best Local Similarity 100.0%; Pred. No. 2.3e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

Db 206 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 238

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

CC designing delivery strategies and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present

CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 424 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 424;

XX

Best Local Similarity 100.0%; Pred. No. 1.6e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

Db 57 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 89

XX

CC RESULT 9

ADJ46292

ID ADJ46292 standard; peptide; 33 AA.

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

CC designing delivery strategies and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present

CC sequence is the predicted sequence of a fragment of the T7 p17 protein.

XX

SQ Sequence 424 AA;

XX

Query Match 100.0%; Score 176; DB 8; Length 573;

XX

Best Local Similarity 100.0%; Pred. No. 2.3e-17;

XX

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 33

XX

Db 57 KNESSNTANTKQWRDETKGFRDEAKRFKNTAG 89

XX

CC RESULT 10

ADJ46292

ID ADJ46292 standard; peptide; 33 AA.

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdkte J, Higgs L;

XX

PI Wakefield D, Sebestyen MG;

XX

DR WPI: 2004-203636/19.

XX

PT Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX

PT a mouse, rat, monkey or human, comprising a T7 ligand attached to

XX

PT compound.

XX

PS Example 3; Page 26; 56pp; English.

XX

CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and potentially utilizes different

CC cellular internalization pathways which allows more flexibility in

Key	Location/Qualifiers
Misc-difference 15	/note= "Wild-type residue replaced with Lys"
WO2004013307-A2.	
PD 12-FEB-2004.	
XX 04-AUG-2003; 2003WO-US024516.	
XX 05-AUG-2002; 2002US-0401167P.	
XX 04-AUG-2003; 2003US-00633808.	
PR (MIRU-) MIRUS CORP.	
PR Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L; Wakefield D, Sebestyen MG;	
XX WPI; 2004-203636/19.	
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a compound.	
XX Disclosure; Page 10; 56pp; English.	
XX WPI; 2004-203636/19.	
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a compound.	
XX Disclosure; Page 10; 56pp; English.	
XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 peptide, such as T7 p17 rod domain (ADJ46278) · ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phage p17 protein ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.	
XX Sequence 33 AA;	
XX Query Match 98.3%; Score 173; DB 8; Length 33;	
XX Best Local Similarity 97.0%; Pred. No. 2e-18;	
XX Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
XX Qy 1 KNEESSTNATNQWRTDETKGFRDEAKRFKNTAG 33	
XX Db 1 KNEESSTNATNQWRTDETKGFRDEAKRFKNTAG 33	
RESULT 11	
ADR69293 ID ADR69293 standard; peptide; 33 AA.	
XX AC ADR69293;	
XX DT 18-NOV-2004 (first entry)	
XX Bacteriophage T7 cholesterol modified cell targetting peptide MC1054.	
XX KW Post-synthetic modification; nuclelease; siRNA; microRNA; cell delivery; small interfering RNA; cell targetting peptide; cholesterol.	
XX OS Enterobacteria phage T7.	
XX FW Key Location/Qualifiers	
XX FT Modified-site 1 /note= "Lys modified with cholesterol chloroformate "	
XX PD US2004167090-A1.	
XX 26-AUG-2004.	
XX PP 19-FEB-2004; 2004US-0072075.	
XX PR 21-FEB-2003; 2003US-0448789P.	
XX PR 18-MAR-2003; 2003US-0455724P.	
XX PA (MONA/) MONAHAN S. D.	
PA (BUDR/) BUDDE R. V. G.	
PA (NADE/) NADE R. V.	
XX WO2004013307-A2.	
XX 12-FEB-2004.	
XX Key Location/Qualifiers	
XX Misc-difference 26	
XX /note= "Wild-type residue replaced with Arg"	

therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (Adu46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phage p17 protein ligand, where ADu46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.

Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;

Best Local Similarity 97.0%; Pred. No. 5.6e-18;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SEQ ID ADJ46300 standard; peptide: 33 AA.

XX AC ADJ46300;

XX DT 06-MAY-2004 (first entry)

XX DE T7 phage p17 protein ligand, SEQ ID 23.

XX KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

XX OS Synthetic.

XX PH WO2004013307-A2.

XX PT 12-FEB-2004.

XX PN 2003WO-US024516.

XX PD 04-AUG-2003; 2003WO-US024516.

XX PR 05-AUG-2002; 2002US-0401167P.

XX PR 04-AUG-2003; 2003US-00633808.

XX WPI; 2004-203636/19.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdk J, Higgs L;

XX DR WPI; 2004-203636/19.

XX PS Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to a compound.

XX Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I)

XX provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in

XX designing delivery strategies and is useful for delivering therapeutic

XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

XX p17 derived peptide, such as T7 p17 rod domain (Adu46278). ADJ46291-

XX ADJ46313 are synthetic peptides derived from the T7 phage p17 protein

XX ligand, where ADJ46291-ADJ46301 have amino acid changes which do not

XX disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid

XX changes which do disrupt hepatocyte targeting.

CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid
CC changes which do disrupt hepatocyte targeting.

XX SQ Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;

Best Local Similarity 97.0%; Pred. No. 5.6e-18;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SEQ ID 1 KNESSTNATNTKQMRDETKGFRDEAKRFKNTAG 33

DB 1 KNESSTNATNTKQMRDETKGFRDEAKRFKNTAG 33

RESULT 15

ADJ46304 standard; peptide: 33 AA.

XX AC ADJ46304;

XX DT 06-MAY-2004 (first entry)

XX DE T7 phage p17 protein ligand-related peptide, SEQ ID 27.

XX KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

XX OS Synthetic.

XX PH WO2004013307-A2.

XX PT 12-FEB-2004.

XX PN 2003WO-US024516.

XX PR 04-AUG-2003; 2003US-0401167P.

XX PR 05-AUG-2002; 2002US-00633808.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Lutdk J, Higgs L;

XX DR WPI; 2004-203636/19.

XX PS Composition useful for delivering a therapeutic cargo to a hepatocyte in

XX a mouse, rat, monkey or human, comprising a T7 ligand attached to a

XX compound.

XX Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a

CC compound. In (I), the compound comprises a drug (interferon). (I)

CC provides better hepatocyte specificity and is useful for delivering therapeutic

CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7

CC p17 derived peptide, such as T7 p17 rod domain (Adu46278). ADJ46291-

CC ADJ46313 are synthetic peptides derived from the T7 phage p17 protein

CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not

CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid

CC changes which do disrupt hepatocyte targeting.

SQ	Sequence 33 AA:
	Query Match 94.9%; Score 167; DB 8; Length 33;
	Best Local Similarity 90.9%; Pred. No. 1.6e-17;
	Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KNESSNTATNTKQWRIDETKGFRDEAKRFKNTAG 33 1 : : : : : :
Db	1 KNESSNTATNTKQWRIDETRGFRDEAKRFKNTAG 33

Scoring table:	BLOSUM62	Alignments
Gapop:	10.0	Gapext: 0.5
Searched:	1612378 seqs, 512079187 residues	
Total number of hits satisfying chosen parameters:	1612378	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing first 45 summaries	
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.	
	SUMMARIES	
Result No.	Query	Description
-	-	-
1	176 100.0	553 1 VTFP BPT7
2	176 100.0	553 2 Q8LTX6
3	170 96.6	553 2 Q8WY17
4	170 96.6	553 2 Q8WY69
5	168 95.5	553 2 Q6WYC3
6	168 95.5	553 2 Q8WYH2
7	164 94.3	553 2 Q8LTX0
8	164 93.2	553 2 Q8LTX1
9	159 90.3	553 2 Q8LTU3
10	157 89.2	553 2 Q8LTW7
11	157 89.2	553 2 Q8LTW9
12	152 86.4	553 2 Q8LTU5
13	152 86.4	553 2 Q8LTU7
14	152 86.4	553 2 Q8LTU8
15	152 86.4	553 2 Q8LTX7
16	152 86.4	553 2 Q8LTY1
17	152 86.4	553 2 Q8LTY2
18	151 85.8	553 2 Q8LTU9
19	151 85.8	553 2 Q8LTW8
20	151 85.8	553 2 Q8LTX3
21	151 85.8	553 2 Q8LTX4
22	151 85.8	553 2 Q8LTX5
23	151 85.8	553 2 Q8LTX8
24	147 83.5	553 2 Q8LTX9
25	147 83.5	553 2 Q8LTU4
26	146 83.0	553 2 Q8LTU0
27	146 83.0	553 2 Q8LTU4
28	146 83.0	557 1 VTFP BPT3
29	146 83.0	558 2 Q8W5T8
30	146 83.0	558 2 Q8S8J8
31	81.8	553 2 Q8LTU2
		RESULT 1
		VTFP BPT7
		STANDARD;
		PRT; 553 AA.
		ID: P03748; AC: P03748;
		DT: 21-JUL-1986 (Rel. 01, Created)
		DT: 21-JUL-1986 (Rel. 01, Last sequence update)
		DT: 05-JUL-2004 (Rel. 44, Last annotation update)
		DB: Tail fiber protein.
		OS: Bacteriophage T7.
		OS: Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
		OC: T7-like viruses.
		OX: NCBI_TaxID=10660;
		RN: [1]
		RP: SEQUENCE FROM N.A.; PubMed=6864790;
		RX: MEDLINE=83241725;
		RA: Dunn J.J., Studier F.W.;
		RT: "Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements.";
		RL: J. Mol. Biol. 166:477-515 (1983).
		CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
		CC: DR: PIR: V01146; CAA24435.1; -
		DR: InterPro: IPR05604; T7 tail fibre.
		DR: Pfam: PF03906; Phage_T7_tail_1.
		KW: SEQUENCE 553 AA; 61572 MW;
		Query Match 100.0%; Score 176; DB 1; Length 553;
		Best Local Similarity 100.0%; Pred. No. 1..3..15; Mismatches 0; Indels 0; Gaps 0;
		Matched 33; Conservative 33;
		Qy : 1 KNESSNTNATKQMDTKEGRDEAKRFONTAG 33
		Db : 186 KNESSNTNATKQMDTKEGRDEAKRFONTAG 218
		RESULT 2
		Q8LTX6
		ID: Q8LTX6;
		AC: Q8LTX6;
		DT: 01-OCT-2002 (TREMBLrel. 22, Created)
		DT: 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
		DT: 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
		DE: Tail fiber protein.
		GN: Name=17.0;

OS	Bacteriophage T7; viruses, no RNA stage; Caudovirales; Podoviridae;	RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
OC	viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;	RT	"Experimental evolution yields hundreds of mutations in a functional
OC	T7-like viruses	RT	viral genome."
NCBI_TaxID=10760;		RL	J. Mol. Evol. 57:241-248 (2003).
OX		DR	EMBL; AY264777; AAP34112.1; -
[1]		DR	InterPro; IPR005604; T7 tail fibre.
RN		DR	PFam; PF03906; Phage_T7_tail; 1
RP	SEQUENCE FROM N.A.;	SEQUENCE	553 AA; 61787 MW; 58E0426D9A74CC11 CRC64;
RX	PubMed=2013B48; PubMed=12019219;	Query Match	96.6%; Score 170; DB 2; Length 553;
EMBL; AF19438; AFM43534.1; -	RT	Best Local Similarity 97.0%; Pred. No. 8.e-15;	
DR	InterPro; IPR005604; T7 tail fibre.	Matches	0; Mismatches 0; Indels 0; Gaps 0;
DR	PFam; PF03906; Phage_T7_tail; 1.	Qy	1 KNEESSTNATNTKQWDETKGFRDEAKRFKNTAG 33
SQ	SEQUENCE 553 AA; 61580 MW; 11A1394FADBD8EAD1 CRC64;	Db	186 KNEESSTNATNTKQWDETKGFRDEAKRFKNTAG 218
/			
RESULT 5			
Q6WYC3	PRELIMINARY;	PRT;	553 AA.
ID	Q6WYC3	PRELIMINARY;	PRT; 553 AA.
AC	Q6WYC3;	PRELIMINARY;	PRT.
NCBI_TaxID=10760;		RT	"Experimental evolution yields hundreds of mutations in a functional
OX		RT	viral genome."
RN		RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RP	SEQUENCE FROM N.A.;	RT	"Experimental evolution yields hundreds of mutations in a functional
RX	PubMed=22990536; PubMed=14629033;	RT	viral genome."
EMBL; AY264776; AAP34058.1; -	DR	EMBL; AY264776; AAP34058.1; -	
DR	InterPro; IPR005604; T7 tail fibre.	DR	InterPro; IPR005604; T7 tail fibre.
SQ	SEQUENCE 553 AA; 61788 MW; 8E754373E814980C CRC64;	Query Match	95.5%; Score 168; DB 2; Length 553;
Qy	1 KNEESSTNATNTKQWDETKGFRDEAKRFKNTAG 33	Best Local Similarity 97.0%; Pred. No. 1.e-14;	
Db	186 KNEESSTNATNTKQWDETKGFRDEAKRFKNTAG 218	Matches	0; Mismatches 1; Indels 0; Gaps 0;
/			
RESULT 6			
Q6WYH2	PRELIMINARY;	PRT;	553 AA.
ID	Q6WYH2	PRELIMINARY;	PRT; 553 AA.
AC	Q6WYH2;	PRELIMINARY;	PRT.
NCBI_TaxID=10760;		RT	"Experimental evolution yields hundreds of mutations in a functional
OX		RT	viral genome."
RN		RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RP	SEQUENCE FROM N.A.;	RT	"Experimental evolution yields hundreds of mutations in a functional
RX	PubMed=22990536; PubMed=14629033;	RT	viral genome."
EMBL; AY264775; AAP24009.1; -	DR	EMBL; AY264775; AAP24009.1; -	
DR	InterPro; IPR005604; T7 tail fibre.	DR	InterPro; IPR005604; T7 tail fibre.
SQ	SEQUENCE 553 AA; 61833 MW; ECF0426C8E74CC13 CRC64;	Query Match	96.6%; Score 170; DB 2; Length 553;
Q6WY69	PRELIMINARY;	PRT;	553 AA.
ID	Q6WY69	PRELIMINARY;	PRT; 553 AA.
AC	Q6WY69;	PRELIMINARY;	PRT.
NCBI_TaxID=10760;		RT	"Experimental evolution yields hundreds of mutations in a functional
OX		RT	viral genome."
RN		RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RP	SEQUENCE FROM N.A.;	RT	"Experimental evolution yields hundreds of mutations in a functional
RX	PubMed=22990536; PubMed=14629033;	RT	viral genome."
EMBL; AY264775; AAP24009.1; -	DR	EMBL; AY264775; AAP24009.1; -	
DR	InterPro; IPR005604; T7 tail fibre.	DR	InterPro; IPR005604; T7 tail fibre.
SQ	SEQUENCE 553 AA; 61833 MW; 58E0426D9A74CC11 CRC64;	Query Match	96.6%; Score 170; DB 2; Length 553;
Q6WY69	PRELIMINARY;	PRT;	553 AA.
ID	Q6WY69	PRELIMINARY;	PRT; 553 AA.
AC	Q6WY69;	PRELIMINARY;	PRT.
NCBI_TaxID=10760;		RT	"Experimental evolution yields hundreds of mutations in a functional
OX		RT	viral genome."
RN		RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RP	SEQUENCE FROM N.A.;	RT	"Experimental evolution yields hundreds of mutations in a functional
RX	PubMed=22990536; PubMed=14629033;	RT	viral genome."
EMBL; AY264775; AAP24009.1; -	DR	EMBL; AY264775; AAP24009.1; -	
DR	InterPro; IPR005604; T7 tail fibre.	DR	InterPro; IPR005604; T7 tail fibre.
SQ	SEQUENCE 553 AA; 61833 MW; 58E0426D9A74CC11 CRC64;	Query Match	96.6%; Score 170; DB 2; Length 553;
Q6WY69	PRELIMINARY;	PRT;	553 AA.
ID	Q6WY69	PRELIMINARY;	PRT; 553 AA.
AC	Q6WY69;	PRELIMINARY;	PRT.
NCBI_TaxID=10760;		RT	"Experimental evolution yields hundreds of mutations in a functional
OX		RT	viral genome."
RN		RA	Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RP	SEQUENCE FROM N.A.;	RT	"Experimental evolution yields hundreds of mutations in a functional
RX	PubMed=22990536; PubMed=14629033;	RT	viral genome."
EMBL; AY264775; AAP24009.1; -	DR	EMBL; AY264775; AAP24009.1; -	
DR	InterPro; IPR005604; T7 tail fibre.	DR	InterPro; IPR005604; T7 tail fibre.
SQ	SEQUENCE 553 AA; 61833 MW; 58E0426D9A74CC11 CRC64;	Query Match	96.6%; Score 170; DB 2; Length 553;

Qy	1 KNESSNTANTKQWRLDETKGPRDEAKRKFNTA 32	Qy	1 KNESSNTANTKQWRLDETKGPRDEAKRKFNTA 32
SQ	SEQUENCE 553 AA; 61832 MW; CE2632DB5E36885F CRC64;	Db	186 KNESSNTANTKQWRLDETKGPRDEAKRKFNTA 217
Query Match	95.5%; Score 168; DB 2; Length 553;	Query Match	95.2%; Score 164; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 1.7e-14;	0; Mismatches 1; Indels 0; Gaps 0;	Best Local Similarity 96.9%; Pred. No. 5.9e-14;	0; Mismatches 1; Indels 0; Gaps 0;
Matches 32; Conservative 0; Gaps 0;	Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	186 KNESSNTANTKQWRLDETKGPRDEAKRKFNTA 218	Db	186 KNESSNTANTKQWRLDETKGPRDEAKRKFNTA 217
RESULT 7		RESULT 9	
Q8LTX0	PRELIMINARY; PRT; 553 AA.	Q8LTU3	PRELIMINARY; PRT; 553 AA.
Q8LTX0; ID		Q8LTU3; ID	
AC		AC	
DT 01-OCT-2002 (TREMBLrel. 22, Created)		DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)		DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		DB	Tail fiber protein.
DB		GN	Name=17.0;
GN		OS	Bacteriophage T7.
OS		OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC		OC	T7-like viruses.
OC		OX	NCBI_TaxID=10760;
OC		RN	[1] _TaxID=10760;
OC		RP	SEQUENCE FROM N.A.
OC		RX	MEDLINE=22013848; PubMed=12019219;
OC		RA	Hahn M.W., Rausher M.D., Cunningham C.W.;
NCBI_TaxID=10760;		RT	"Distinguishing between selection and population expansion in an
RN [1]		RT	experimental lineage of bacteriophage T7.";
RP		RL	Genetics 161:11-20(2002).
SEQUENCE FROM N.A.		DR	EMBL; AF419510; AAH43606.1; -
MEDLINE=22013848; PubMed=12019219;		DR	InterPro; IPR005604; T7-tail_fibre.
RA		DR	DR
Hahn M.W., Rausher M.D., Cunningham C.W.;		SEQUENCE FROM N.A.	Protein; PF03906; Phage_T7-tail_1;
"Distinguishing between selection and population expansion in an		DR	SEQUENCE 553 AA; 61952 MW; E3DBB0B02A2DAPP2 CRC64;
experimental lineage of bacteriophage T7.";		DR	Query Match 90.3%; Score 159, DB 2; Length 553;
DR		DR	Best Local Similarity 93.8%; Pred. No. 2.9e-13;
EMBL; AF419444; AAH43540.1; -		DR	Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
InterPro; IPR005604; T7-tail_fibre.		DR	Query Match 90.3%; Score 159, DB 2; Length 553;
DR		DR	Best Local Similarity 93.8%; Pred. No. 2.9e-13;
PFam; PF03906; Phage_T7-tail_1;		DR	Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
SEQUENCE 553 AA; 61829 MW; 8B995AA3956CDC89 CRC64;		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
SQ		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
OC		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
OC		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
OC		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
OC		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
OC		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
OC		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
OC		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
OC		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
OC		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NCBI_TaxID=10760;		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
RN [1]		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
RP		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQUENCE FROM N.A.		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
MEDLINE=22013848; PubMed=12019219;		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
RA		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Hahn M.W., Rausher M.D., Cunningham C.W.;		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
"Distinguishing between selection and population expansion in an		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
experimental lineage of bacteriophage T7.";		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
EMBL; AF41943; AAH43539.1; -		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
InterPro; IPR005604; T7-tail_fibre.		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PFam; PF03906; Phage_T7-tail_1;		DR	Query Match 89.2%; Score 157, DB 2; Length 553;
SEQUENCE 553 AA; 61753 MW; ADA80C4B2B5BDB16 CRC64;		DR	Best Local Similarity 93.8%; Pred. No. 5.4e-13;
SQ		DR	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11	Q8LTW9	PRELIMINARY;	PRT;	553 AA.	DT 01-OCT-2002 (TREMBLrel. 22, Created)	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DE Tail fiber protein.
	AC Q8LTW9;				GN Name=17.0;					
	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)				OS Bacteriophage T7.					
	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)				OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;					
	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)				OC T7-like viruses.					
	DE Tail fiber protein.				OX NCBI_TaxID=10760;					
	GN Name=17.0;				RN [1]					
	OS dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;				RP SEQUENCE FROM N.A.					
	OC T7-like viruses.				RX MEDLINE=22013848; PubMed=12019219;					
	OX NCBI_TaxID=10760;				RA Hahn M.W., Rausher M.D., Cunningham C.W.;					
	RN [1]				RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";					
	RP SEQUENCE FROM N.A.				RL Genetics 161:11-20(2002).					
	RX MEDLINE=22013848; PubMed=12019219;				DR EMBL; AF419506; AAC3602.1;					
	RA Hahn M.W., Rausher M.D., Cunningham C.W.;				DR InterPro; IPR005604; T7-tail_fibre.					
	RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";				DR Pfam; PF03906; Phage_T7-tail; 1.					
	RL Genetics 161:11-20(2002).				SQ SEQUENCE 553 AA; 62052 MW; E03509AFAADA3EC CRC64;					
	DR EMBL; AF419445; AAC4341.1; -				Query Match Score 152; DB 2; Length 553;					
	DR InterPro; IPR005604; T7-tail_fibre.				Best Local Similarity 90.6%; Pred. No. 2.6e-12;					
	DR Pfam; PF03906; Phage_T7-tail; 1.				Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
	SQ SEQUENCE 553 AA; 61805 MW;				Qy 1 KNESSNTANTKQWDRDETKGFRDEAKRFKNTA 32					
	Query Match Score 157; DB 2; Length 553;				Db 186 KDESSTNATNTKQWDRDEIKFRDEAKRFKNTA 217					
	Best Local Similarity 93.8%; Pred. No. 5.4e-13;				RESULT 14					
	Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				Q8LTU8 PRELIMINARY; PRT; 553 AA.					
	Qy 1 KNESSNTANTKQWDRDETKGFRDEAKRFKNTA 32				DB Q8LTU8 ID Q8LTU8 PRELIMINARY; PRT; 553 AA.					
	Db 186 KDESSTNATNTKQWDRDEIKFRDEAKRFKNTA 217				AC Q8LTU8 ID Q8LTU8 PRELIMINARY; PRT; 553 AA.					
	RESULT 12				DR Q8LTU8 ID Q8LTU8 PRELIMINARY; PRT; 553 AA.					
	Q8LTU5	PRELIMINARY;	PRT;	553 AA.	DT 01-OCT-2002 (TREMBLrel. 22, Created)	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DE Tail fiber protein.
	AC Q8LTU5;				GN Name=17.0;					
	DT 01-OCT-2002 (TREMBLrel. 22, Created)				OS Bacteriophage T7.					
	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)				OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;					
	DE Tail fiber protein.				OC T7-like viruses.					
	GN Name=17.0;				OX NCBI_TaxID=10760;					
	OS Bacteriophage T7.				RN [1]					
	OC T7-like viruses.				RP SEQUENCE FROM N.A.					
	OX NCBI_TaxID=10760;				RX MEDLINE=22013848; PubMed=12019219;					
	RN [1]				RA Hahn M.W., Rausher M.D., Cunningham C.W.;					
	RP SEQUENCE FROM N.A.				RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";					
	RX MEDLINE=22013848; PubMed=12019219;				RL Genetics 161:11-20(2002).					
	RA Hahn M.W., Rausher M.D., Cunningham C.W.;				DR EMBL; AF419506; AAC3601.1; -					
	RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";				DR InterPro; IPR005604; T7-tail_fibre.					
	RL Genetics 161:11-20(2002).				DR Pfam; PF03906; Phage_T7-tail; 1.					
	DR EMBL; AF419508; AAC4304.1; -				SQ SEQUENCE 553 AA; 62303 MW; 5868AAE851F700CC CRC64;					
	DR InterPro; IPR005604; T7-tail_fibre.				Query Match Score 152; DB 2; Length 553;					
	DR Pfam; PF03906; Phage_T7-tail; 1.				Best Local Similarity 90.6%; Pred. No. 2.6e-12;					
	SQ SEQUENCE 553 AA; 62184 MW;				Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
	Query Match Score 152; DB 2; Length 553;				Qy 1 KNESSNTANTKQWDRDETKGFRDEAKRFKNTA 32					
	Best Local Similarity 90.6%; Pred. No. 2.6e-12;				Db 186 KDESSTNATNTKQWDRDEIKFRDEAKRFKNTA 217					
	Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				RESULT 15					
	Qy 1 KNESSNTANTKQWDRDETKGFRDEAKRFKNTA 32				Q8LTX7 PRELIMINARY; PRT; 553 AA.					
	Db 186 KDESSTNATNTKQWDRDEIKFRDEAKRFKNTA 217				AC Q8LTX7 ID Q8LTX7 PRELIMINARY; PRT; 553 AA.					
	AC Q8LTU7				DR Q8LTU7 ID Q8LTU7 PRELIMINARY; PRT; 553 AA.					
	AC Q8LTU7;				DT 01-OCT-2002 (TREMBLrel. 22, Created)					
	AC Q8LTU7;				DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
	AC Q8LTU7;				DE Tail fiber protein.					
	AC Q8LTU7;				GN Name=17.0;					

OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W.; Rausher M.D.; Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
experimental lineage of bacteriophage T7.";
RT Generics 161:11-20(2002).
RL EMBL; AR419431; AAM43533.1;
DR IPR005604; T7 tail fibre.
DR InterPro; PF03906; Phage_T7-tail_1.
DR Pfam; PF03906; Phage_T7-tail_1.
SQ SEQUENCE 553 AA; 62029 MW; 880653CDF5C4FBB9 CRC64;
Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 KNESSNTNATNKQWDETKGPRDEAKRFNTA 32
Db 186 KDESSTNATNKQWDETKGPRDEAKRFNTA 217

Search completed: March 30, 2005, 14:37:06
Job time : 190 SECs

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ALIGNMENTS							
Searched: 283416 seqs, 96216763 residues							
Total number of hits satisfying chosen parameters: 283416							
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
Database : PIR79:*							
1: PIR1:*							
2: PIR2:*							
3: PIR3:*							
4: PIR4:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	176	100.0	553	1	TLBPF7	tail fiber protein	RESULT 1
2	146	83.0	557	1	TLBPT3	tail fiber protein	TLBPF7
3	61	34.7	879	2	S49910	chloroplast outer	C;Species: phage T7
4	60	34.7	1662	1	H71402	hypothetical protein	C;Accession: A04373
5	57	32.4	186	2	AH2450	hypothetical protein	A;Molecule type: DNA
6	57	32.4	509	2	AB2496	transposase a	A;Residues: 1-553 <DUN>
7	56.5	32.1	3079	1	RGBY12	probable GRPase-ac	A;Cross-references: UNIPROT: P03748
8	55	31.2	466	2	T07404	probable Glucosylt	R;Dunn, J.J.; Studier, F.W.
9	54	30.7	346	2	G87440	rod shape-determin	J. Mol. Biol. 166, 477-535, 1983
10	53	30.1	167	2	S46656	ubiquitin-protein	A;Reference number: 943393
11	53	30.1	880	2	T48470	hypothetical protein	A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the location
12	52	29.5	69	2	A82489	cold shock DNA-bm	A;Accession: S42283; MUID: 6864725; PMID: 83241725
13	52	29.5	169	2	T02243	cold shock DNA-conjugat	A;Cross-references: EMBL: 701146; NCBI: 9431187; PID: CAA24435.1; PMID: 915611
14	51.5	29.3	174	2	AD2666	conserved hypothetical	A;Note: the authors did not translate the codon for residue 1
15	51.5	29.3	192	2	B97448	immuno-reactive 14K	C;Genetics:
16	51	29.0	166	2	S71209	ubiquitin-protein	C;Keywords: tail fiber protein
17	51	29.0	573	2	F81113	peptidase 'M3' fami	C;Superfamily: phage T7 tail fiber
18	50.5	28.7	648	2	A83792	acetyl-CoA synthet	C;Accession: A04373
19	50	28.4	136	2	A96305	uncharacterized sm	A;Note: host Escherichia coli
20	50	28.4	476	2	T03745	glucosyltransferases	C;Date: 31-Dec-1988 #sequence_revision
21	50	28.4	751	2	B87391	TobB-dependent rec	C;Accession: A23476
22	50	28.4	960	2	AF1940	isoleucyl-tRNA syn	A;Residues: 1-557 <YAM>
23	50	28.4	2481	2	D90011	FmbB protein [imp	A;Cross-references: UNIPROT: P01308; GB: M14784; PID: 62215810; PMID: 86209997; MUID: 3010556
24	50	28.4	3328	2	T30335	breast cancer tumo	A;Title: Cloning and sequencing of the genetic right end of bacteriophage T3 D
25	50	28.4	3329	2	T42205	breast cancer susc	A;Accession: S42233
26	50	28.4	3329	2	T30504	breast cancer tumo	A;Cross-references: EMBL: 701146; NCBI: 943393; MUID: 6864725; PMID: 83241725
27	49	27.8	70	2	E82399	cold shock domain	A;Molecule type: DNA
28	49	27.8	298	2	S50735	hypothetical prote	A;Residues: 1-557 <YAM>
29	49	27.8	336	2	GB1152	probable DNA bindi	A;Cross-references: UNIPROT: P01308; GB: M14784; PID: 62215810; PMID: 86209997; MUID: 3010556

R; Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.
 Virology 154, 246, 1986
 A; Reference number: A94344
 A; Contents: annotation; erratum; corrections to coding regions
 C; Genetics:
 A; Gene: 17
 C; Superfamily: phage T7 tail fiber protein
 C; Keywords: tail fiber

Query Match 83.0%; Score 146; DB 1; Length 557;
 Best Local Similarity 81.8%; Pred. No. 8.2e-12;
 Matches 27; Conservative 2; Mismatches 14; Indels 0; Gaps 0; Gaps 0;

Db 186 KNEGTINATNTKQWRDTKGFDEAKRFKNTAG 33

RESULT 3
 S49910 outer envelope protein OEP86 precursor - garden pea
 N; Alternate names: chloroplast import-associated protein IAP86, GTP-binding
 C; Species: *Pisum sativum* (garden pea)
 C; Accession: S49910; A55366; A55171
 R; Hirsch, S.; Soil, J.
 A; Reference number: S49910
 A; Accession: S49910
 A; Molecule type: mRNA
 A; Residues: 1-879 <HR>
 A; Cross-references: UNIPROT:Q41010; EMBL:231581; NID:9599957; PMID:9599958
 R; Hirsch, S.; Muckel, E.; Heemeyer, F.; von Heijne, G.; Soil, J.
 A; Title: A receptor component of the chloroplast protein translocation machinery.
 A; Reference number: A55386; MUID:95099322; PMID:7801125
 A; Accession: A55386
 A; Status: nucleic acid sequence not shown
 A; Molecule type: mRNA
 A; Residues: 1-137, 'Q', 139-875, 877-879 <HR>
 R; Kessler, F.; Blobel, G.; Patel, H.A.; Schnell, D.J.
 Science 266, 105-109, 1994
 A; Title: Identification of two GTP-binding proteins in the chloroplast protein import machinery.
 A; Reference number: A55171; MUID:95063938; PMID:7973656
 A; Accession: A55171
 A; Molecule type: mRNA
 A; Residues: 1-372, 'EQ', 376-879 <KBS>
 A; Cross-references: GB:L36857; NID:5676508; PMID:953276.1; PID:9576509
 C; Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; P-loop
 F; 245-252/Region: nucleotide-binding motif A (P-loop)

Query Match 83.0%; Score 146; DB 1; Length 557;
 Best Local Similarity 81.8%; Pred. No. 8.2e-12;
 Matches 27; Conservative 2; Mismatches 14; Indels 0; Gaps 0; Gaps 0;

Db 186 KNEGTINATNTKQWRDTKGFDEAKRFKNTAG 33

RESULT 4
 H71402 probable kinesin - *Arabidopsis thaliana* (mouse-ear cress)
 C; Species: *Arabidopsis thaliana* (mouse-ear cress)
 A; Variety: Columbia
 C; Accession: H71402
 R; Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, B.; Wambutt, R.; Weitzenseger, T.; Pohl, T.M.; Terry, N.; Giel vananagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Puigdomenech
 erhoft, A.; Moores, T.; Jones, J.D.G.; Enava, T.; Palme, K.; Benes, V.; Rechman, S.; Ans

C.; Chalwatzi, N.; Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thaliana* - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
 A; Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thaliana* - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
 A; Reference number: A71400; MUID:946125
 A; Accession: H71402
 C; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-1662 <BEV>
 A; Cross-references: UNIPROT:Q23274; GB:297335; NID:92244747; PIDN:CA810194.1; PID:922447
 C; Genetics:
 A; Map position: 4C0P9-4C3845
 C; Superfamily: Arabidopsis thaliana 186.9K kinesin-related protein; kinesin motor domain homology <RMOT>
 F; 43-423/Domain: kinesin motor domain homology <RMOT>
 Query Match 34.1%; Score 60; DB 1; Length 1662;
 Best Local Similarity 40.0%; Pred. No. 9.7%;
 Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
 Gaps 0;
 Qy 3 ESSTNATNTKQWRDTKGFDEAKRFKNTA 32
 Db 1241 EPSVNASSEQQWRDDEPELYKKTFSNL A 1270

RESULT 5
 AH2450 hypothetical protein alr5160 [imported] - *Nostoc* sp. (strain PCC 7120)
 C; Species: *Nostoc* sp. (strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120)
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C; Date: 14-Dec-2001 #text_change 09-Jul-2004
 C; Accession: AH2450
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, S.; DNA Res. 8, 205-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A; Reference number: AB1807; MUID:21595285; PMID:11759840
 A; Accession: AH2450
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-186 <KUR>
 A; Cross-references: UNIPROT:Q8YLY6; GB:BA000019; PIDN:BA876859.1; PID:917134298; GSPDB:G
 A; Experimental source: strain PCC 7120
 C; Genetics:
 A; Gene: alr5160
 C; Superfamily: uncharacterized conserved protein *ssr2962*
 Query Match 32.4%; Score 57; DB 2; Length 186;
 Best Local Similarity 68.8%; Pred. No. 2.3%;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Gaps 0;
 Qy 5 STNATNTKQWRDTKGF 20
 Db 94 STFTIAKQWRDTK 109

RESULT 6
 AB2496 transposase alr7147 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120alpha
 C; Species: *Nostoc* sp. (strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120)
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C; Date: 14-Dec-2001 #text_change 09-Jul-2004
 C; Accession: AB2496
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, S.; DNA Res. 8, 205-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A; Reference number: AB1807; MUID:21595285; PMID:11759840
 A; Accession: AB2496
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-509 <KUR>
 A; Cross-references: UNIPROT:Q8YKZ2; GB:BA000020; PIDN:BA878230.1; PID:917135684; GSPDB:G
 A; Experimental source: strain PCC 7120
 C; Genetics:
 A; Gene: alr7147

A;Genome: plasmid

Query Match 32.4%; Score 57; DB 2; Length 509;

Best Local Similarity 55.6%; Pred. No. 6.8;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 13 QWRDETKFRDEAKRFKN 30

Db 331 QWLDKURRSFRDLSKGFKN 348

RESULT 7

RGYI2 probable GTPase-activating protein IRA2 - yeast (Saccharomyces cerevisiae) N;Alternate names: G14 protein, protein 00985; protein YOL0951

C;Species: Saccharomyces cerevisiae

C;Accession: S66775; S66774; A5656; S4854; S5042; S1190; S38505

R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66775

A;Accession: S66775

A;Molecule type: DNA

A;Residues: 1-243 <ZUM>

A;Cross-references: UNIPROT:PI19158; UNIPROT:O13592; EMBL:Z74823; GSPDB:GN00015; MIPS:YOL0951

A;Experimental source: strain S288C

A;Gene: twi1

A;Genetics:

A;Keywords: flavonol 03-glucosyltransferase; hexosyltransferase

A;Reference number: S66756

A;Accession: S66774

A;Molecule type: DNA

A;Residues: 1983-3079 <ALE>

A;Cross-references: EMBL:Z74823; GSPDB:GN00015; MIPS:YOL081W

A;Experimental source: strain S288C

A;Title: IRA2, a second gene of Saccharomyces cerevisiae that encodes a protein with a domain of unknown function

A;Reference number: S48253; MUID:95208358; PMID:7900427

A;Accession: A35656; MUID:90318397; PMID:2164637

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-2308; 'V', 2310-2316, 'I', 2318-3079 <TAN>

A;Cross-references: EMBL:MS3777; NID:9171761; PID:9171762

R;Zumstein, E.; Griffin, H.; Schweizer, M.

Yeast 10, 1383-1387, 1994

A;Title: Sequence of a 10.27 kb segment on the left arm of chromosome XV from Saccharomyces cerevisiae

A;Reference number: S48253; MUID:95208358; PMID:7900427

A;Accession: S48254

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-2423 <ZUM>

A;Cross-references: EMBL:X75441; NID:941079; PID:CAA53202; PID:9414081

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

submitted to the EMBL Data Library, December 1994

A;Reference number: S50410

A;Accession: S50426

A;Molecule type: DNA

A;Residues: 1-2423 <ZUM>

A;Cross-references: EMBL:X83121; NID:9600461; PID:9600480

C;Genetics:

A;Gene: SGD:IRA2; MIPS:YOL081W

A;Cross-references: SGD:S0005441; MIPS:YOL081W

A;Map position: 15L

C;Superfamily: regulatory protein IRA2; ras-specific GAP catalytic domain homology

C;Keywords: transmembrane protein

F;693-709/Domain: transmembrane #status predicted <TM1>

F;1135-1151/Domain: transmembrane #status predicted <TM2>

F;1701-1910/Domain: ras-specific GAP catalytic domain homology <TM2>

F;1842-1858/Domain: transmembrane #status predicted <TM3>

F;2318-2334/Domain: transmembrane #status predicted <TM4>

F;2562-2578/Domain: transmembrane #status predicted <TM5>

RESULT 8

T07404 probable glucosyltransferase twi1 (BC 2.4.1.-) - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

R;Truesdale, M.R.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z16014

A;Accession: T07404

A;Status: translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-466 <TRU>

A;Cross-references: UNIPROT:Q43526; EMBL:X85138; PID:9971438

A;Experimental source: cultivar Moneymaker; wounded leaf

C;Keywords: glycosyltransferase; hexosyltransferase

A;Gene: twi1

A;Genetics:

Query Match 32.1%; Score 56.5; DB 1; Length 3079;

Best Local Similarity 32.6%; Pred. No. 5.6;

Matches 15; Conservative 9; Mismatches 7; Indels 15; Gaps 2;

Qy 2 NESSNTATNT----KQRDETK-----GFRDEAKRFKNTA 32

Db 2296 NNSSTSSPNSNNKDDQKQERTKLLCHILLVSLIGLDESKMKNS 2341

RESULT 9

G87440 rod shape-determining protein MreC [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: G87440

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Haff, D.H.; Kollar, J.J.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173638; PMID:11259647

A;Accession: G87440

C;Superfamily: rod shape-determining protein mreC

Query Match 30.7%; Score 54; DB 2; Length 346;

Best Local Similarity 40.9%; Pred. No. 11;

Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 12 KQRDETKGFRDEAKRFKNTAG 33

Db 100 RQRDRALQDQNRKPSLIG 121

RESULT 10

S46656 ubiquitin-protein ligase (EC 6.3.2.19) UBC14 [similarity] - Arabidopsis thaliana

N;Alternate names: ubiquitin carrier protein E2 (clone TAY029); ubiquitin-conjugating enzyme (EC 6.3.1.1)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 14-Jul-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
 C;Accession: S4656; T4767; T51255; S59844
 R;Genochik, P.; Durr, A.; Fleck, J.
 MOL; Gen. Genet. 244, 548-556, 1994
 A;Title: Differential expression of several B2-type ubiquitin carrier protein genes at d
 A;Reference number: S46656; MUID:94359481; PMID:8078482
 A;Accession: S46656
 A;Molecule type: mRNA
 A;Residues: 1-167 <GNN>
 A;Cross-references: UNIPROT:PA2747; EMBL:X72625; NID:9600388; PIDN:CAA51200.1; PID:96003
 R;Bensch, V.; Wurmback, E.; Drzonek, R.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24472
 A;Accession: T4767
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-167 <GNN>
 A;Cross-references: EMBL:AL132975
 A;Experimental source: cultivar Columbia; BAC clone T22B16
 R;van Nicker, S.; Walker, J.M.; Vierstra, R.D.
 J; Biol. Chem. 271:12150-12158, 1996
 A;Title: The Arabidopsis thaliana UBC7/13/14 genes encode a family of multiubiquitin chaperones
 A;Accession: T51255
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Cross-references: EMBL:U33755; PIDN: AAC49323.1
 C;Genetics:
 A;Gene: UBC14
 A;Map Position: 3
 A;Introns: 16/1; 50/2; 83/1; 116/3
 A;Note: T22B16.40
 C;Superfamily: human ubiquitin-protein ligase E2
 C;Keywords: ligase

RESULT 12
 A82489
 cold shock DNA-binding domain protein VCA0184 [imported] - *Vibrio cholerae* (strain N1696
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Embley, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.;
 R.; R.R.; Mekalanos, J.C.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82489
 A;Accession: A82489
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-69 <HEI>
 A;Cross-references: UNIPROT:Q9KMY2; GB:AE004359; PIDN:99557575; PIDN:AAF9609
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCA0184
 A;Map Position: 2
 C;Superfamily: cold shock protein; cspa type; cold shock domain homology
 Query Match 29.5%; Score 52; DB 2; Length 69;
 Best Local Similarity 58.8%; Pred. No. 3.7;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 5 STNATNTKQWRDETKG 21
 Db 2 STPVTGTVKWNFNETKG 18

RESULT 13
 T02943
 ubiquitin-conjugating enzyme - maize
 N;Alternative names: ubiquitin carrier protein
 C;Species: Zea mays (maize)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02943
 R;de Vries, A.; Corotis, S.; Dresselhaus, T.
 Plant Physiol. 118: 1101, 1998
 A;Title: Molecular Characterization of a cDNA Encoding an Ubiquitin Carrier Protein (UBC)
 A;Reference number: Z14787; MUID:990811; PMID:990811
 A;Accession: T02943
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-169 <DEV>
 C;Cross-references: UNIPROT:Q24560; EMBL:AJ002959; PIDN:CAA05772.1
 C;Superfamily: human ubiquitin-protein ligase E2
 Query Match 29.5%; Score 52; DB 2; Length 169;
 Best Local Similarity 30.8%; Pred. No. 9.7;
 Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 Qy 2 NESSTNTNTKQWRDETKG 27
 Db 135 DESPANTAAKEWREQREDPKKKVRR 160

RESULT 14
 AD2666
 conserved hypothetical protein Atu0730 [imported] - *Agrobacterium tumefaciens* (strain C5
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
 erage, G.; Gillet, J.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.

C;Genetics:
 A;Map Position: 5
 A;Introns: 3/06/3; 349/2; 396/2; 425/2; 476/3; 639/3; 735/2; 778/3
 A;Note: T1E3.170
 Query Match 30.1%; Score 53; DB 2; Length 880;
 Best Local Similarity 30.3%; Pred. No. 42;
 Matches 10; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
 Qy 1 KNESSNTNTKQWRDETKGFRDEAKRFKNTAG 33
 Db 259 EGEDDTKMSNKSWHQREGSRSLQRILDING 291

A. Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58
A. Reference number: AB2377; MVID:21608550; PMID:11743193
A. Accession: AD2666
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-174 <DNA>
A. Cross-references: UNIPROT:Q8UHF2; GB:AE008688; PIDN:AAL41746.1; PID:917739097; GDB:39097
A. Experimental source: strain C58 (Dupont)
C. Genetics:
A. Gene: Atu0730
A. Map position: circular chromosome

RESULT 15
B97448 Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Accession: B97448 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Reference number: 21604551. MITB:174743194

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Search time: 54 seconds

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